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SEQUENCE LISTING



<110> Borriello, Francescopaolo
Band, Hamid

<120> Characterization of a novel gene Cbl-SL

<130> B0801/7159/ERP

<140> 09/434,708

<141> 1999-11-05

<150> U.S. 60/107,470

<151> 1998-11-06

<160> 10

<170> FastSEQ for Windows Version 3.0

<210> 1

<211> 1547

<212> DNA

<213> Homo Sapiens

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<221> CDS

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Glu Ala Arg Ala Leu Gly Arg Ala Val Arg Met Leu Gln Arg Leu Glu
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gag caa tgc gtc gac ccc cgg ctg tcc gtg agt ccc cct tcg ctg cgg 147
Glu Gln Cys Val Asp Pro Arg Leu Ser Val Ser Pro Pro Ser Leu Arg
30 35 40 45

gac ctg ctg ccc cgc aca gcg cag ctg ctt cga gag gtg gcc cat tct 195
Asp Leu Leu Pro Arg Thr Ala Gln Leu Arg Glu Val Ala His Ser
50 55 60

cgg cgg gcg gcc ggc gga ggc ggc ccc ggg ggt ccc ggc ggc tct ggg 243
Arg Arg Ala Ala Gly Gly Gly Gly Pro Gly Gly Pro Gly Gly Ser Gly
65 70 75

gac ttt cta ctc atc tac ctg gcc aat ctg gag gcc aag agc agg cag 291
Asp Phe Leu Leu Ile Tyr Leu Ala Asn Leu Glu Ala Lys Ser Arg Gln
80 85 90

gtg gcc gcg ctg ctg cct ccc cgg ggc cga agg agt gcc aac gac gag 339
Val Ala Ala Leu Leu Pro Pro Arg Gly Arg Arg Ser Ala Asn Asp Glu
95 100 105

ctc ttc cgg gcg ggc tcc aga ctc agg cga cag ctg gcc aag ctg gcc 387
Leu Phe Arg Ala Gly Ser Arg Leu Arg Arg Gln Leu Ala Lys Leu Ala

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atc atc ttc agc cac atg cac gca gag ctg cac gca ctc ttc ccc ggg Ile Ile Phe Ser His Met His Ala Glu Leu His Ala Leu Phe Pro Gly	130	135	140	435
gca aag tac tgt gga cac atg tac cag ctc acc aag gcc ccc gcc cac Ala Lys Tyr Cys Gly His Met Tyr Gln Leu Thr Lys Ala Pro Ala His	145	150	155	483
acc ttc tgg agg gaa agt tgc gga gcc cgg tgt gtg ctg ccc tgg gct Thr Phe Trp Arg Glu Ser Cys Gly Ala Arg Cys Val Leu Pro Trp Ala	160	165	170	531
gag ttt gag tcc ctc ctg ggc acc tgc cac cct gtg gaa cca ggc tgc Glu Phe Glu Ser Leu Leu Gly Thr Cys His Pro Val Glu Pro Gly Cys	175	180	185	579
aca gcc ctg gcc ttg cgc acc acc att gac ctc acc tgc agc ggg cac Thr Ala Leu Ala Leu Arg Thr Thr Ile Asp Leu Thr Cys Ser Gly His	190	195	200	627
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cca aca ctc ctc aag aac tgg cag ctc ctg gca gtc aac cac cca ggc Pro Thr Leu Leu Lys Asn Trp Gln Leu Ala Val Asn His Pro Gly	225	230	235	723
tac atg gcc ttc ctc acc tat gat gag gtc caa gag cgt ctg cag gcc Tyr Met Ala Phe Leu Thr Tyr Asp Glu Val Gln Glu Arg Leu Gln Ala	240	245	250	771
tgc agg gac aag cca ggc agt tac atc ttc cgg ccc agc tgt act cgc Cys Arg Asp Lys Pro Gly Ser Tyr Ile Phe Arg Pro Ser Cys Thr Arg	255	260	265	819
ctg ggg cag tgg gcc atc ggc tat gtg agc tca gat ggc agc atc ctg Leu Gly Gln Trp Ala Ile Gly Tyr Val Ser Ser Asp Gly Ser Ile Leu	270	275	280	867
cag acc atc cct gcc aac aaa ccc ctg tcc cag gtg ctc ctg gag gga Gln Thr Ile Pro Ala Asn Lys Pro Leu Ser Gln Val Leu Leu Gly	290	295	300	915
cag aag gac ggc ttc tac ctc tac cca gat gga aag acc cac aac cca Gln Lys Asp Gly Phe Tyr Leu Tyr Pro Asp Gly Lys Thr His Asn Pro	305	310	315	963
gac ctg act gag ctc ggc cag gca gaa ccc cag cag cgc atc cac gtg Asp Leu Thr Glu Leu Gly Gln Ala Glu Pro Gln Gln Arg Ile His Val	320	325	330	1011
tca gag gag cag ctg cag ctc tac tgg gcc atg gac tcc aca ttt gag Ser Glu Glu Gln Leu Gln Leu Tyr Trp Ala Met Asp Ser Thr Phe Glu	335	340	345	1059
ctc tgc aag atc tgt gct gag agc aac aag gat gtg aag att gag ccg Leu Cys Lys Ile Cys Ala Glu Ser Asn Lys Asp Val Lys Ile Glu Pro	350	355	360	1107

B¹
nt

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385 390 395	

gcc gtg agt atc tac cag ttc cac ggt cag gct act gct gag gac tca	1251
Ala Val Ser Ile Tyr Gln Phe His Gly Gln Ala Thr Glu Asp Ser	
400 405 410	

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Gly Asn Ser Ser Asp Gln Glu Gly Arg Glu Leu Glu Leu Gly Gln Val	
415 420 425	

ccc ctt tcg gct cct cca ttg ccc cca cgg cca gat ctg ccc ccc agg	1347
Pro Leu Ser Ala Pro Pro Leu Pro Pro Arg Pro Asp Leu Pro Pro Arg	
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Lys Pro Arg Asn Ala Gln Pro Lys Val Arg Leu Leu Lys Gly Asn Ser	
450 455 460	

cct cca gct gcg ctg gga ccc cag gac cct gcc ccg gcc tgaaggccag	1444
Pro Pro Ala Ala Leu Gly Pro Gln Asp Pro Ala Pro Ala	
465 470	

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Pro Arg Thr Ala Gln Leu Leu Arg Glu Val Ala His Ser Arg Arg Ala	
50 55 60	
Ala Gly Gly Gly Gly Pro Gly Gly Pro Gly Gly Ser Gly Asp Phe Leu	
65 70 75 80	
Leu Ile Tyr Leu Ala Asn Leu Glu Ala Lys Ser Arg Gln Val Ala Ala	
85 90 95	
Leu Leu Pro Pro Arg Gly Arg Arg Ser Ala Asn Asp Glu Leu Phe Arg	
100 105 110	
Ala Gly Ser Arg Leu Arg Arg Gln Leu Ala Lys Leu Ala Ile Ile Phe	
115 120 125	
Ser His Met His Ala Glu Leu His Ala Leu Phe Pro Gly Ala Lys Tyr	
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Cys Gly His Met Tyr Gln Leu Thr Lys Ala Pro Ala His Thr Phe Trp	
145 150 155 160	
Arg Glu Ser Cys Gly Ala Arg Cys Val Leu Pro Trp Ala Glu Phe Glu	
165 170 175	
Ser Leu Leu Gly Thr Cys His Pro Val Glu Pro Gly Cys Thr Ala Leu	

180 185 190
 Ala Leu Arg Thr Thr Ile Asp Leu Thr Cys Ser Gly His Val Ser Ile
 195 200 205
 Phe Glu Phe Asp Val Phe Thr Arg Leu Phe Gln Pro Trp Pro Thr Leu
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 Leu Lys Asn Trp Gln Leu Leu Ala Val Asn His Pro Gly Tyr Met Ala
 225 230 235 240
 Phe Leu Thr Tyr Asp Glu Val Gln Glu Arg Leu Gln Ala Cys Arg Asp
 245 250 255
 Lys Pro Gly Ser Tyr Ile Phe Arg Pro Ser Cys Thr Arg Leu Gly Gln
 260 265 270
 Trp Ala Ile Gly Tyr Val Ser Ser Asp Gly Ser Ile Leu Gln Thr Ile
 275 280 285
 Pro Ala Asn Lys Pro Leu Ser Gln Val Leu Leu Glu Gly Gln Lys Asp
 290 295 300
 Gly Phe Tyr Leu Tyr Pro Asp Gly Lys Thr His Asn Pro Asp Leu Thr
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 Glu Leu Gly Gln Ala Glu Pro Gln Gln Arg Ile His Val Ser Glu Glu
 325 330 335
 Gln Leu Gln Leu Tyr Trp Ala Met Asp Ser Thr Phe Glu Leu Cys Lys
 340 345 350
 Ile Cys Ala Glu Ser Asn Lys Asp Val Lys Ile Glu Pro Cys Gly His
 355 360 365
 Leu Leu Cys Ser Cys Cys Leu Ala Ala Trp Gln His Ser Asp Ser Gln
 370 375 380
 Thr Cys Pro Phe Cys Arg Cys Glu Ile Lys Gly Trp Glu Ala Val Ser
 385 390 395 400
 Ile Tyr Gln Phe His Gly Gln Ala Thr Ala Glu Asp Ser Gly Asn Ser
 405 410 415
 Ser Asp Gln Glu Gly Arg Glu Leu Glu Leu Gly Gln Val Pro Leu Ser
 420 425 430
 Ala Pro Pro Leu Pro Pro Arg Pro Asp Leu Pro Pro Arg Lys Pro Arg
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